



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 03:24 PM UTC

PDB ID : 3AZ8 / pdb_00003az8
Title : Beta-Hydroxyacyl-Acyl Carrier Protein Dehydratase (FabZ) from Plasmodium falciparum in complex with NAS21
Authors : Maity, K.; Venkata, B.S.; Kapoor, N.; Surolia, N.; Surolia, A.; Suguna, K.
Deposited on : 2011-05-20
Resolution : 3.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

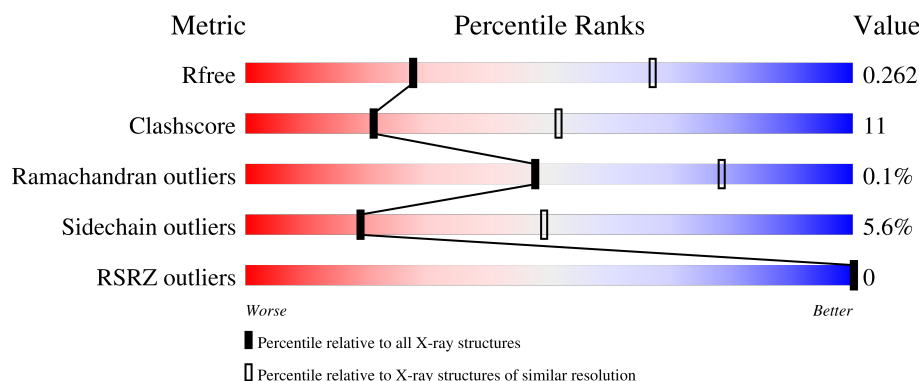
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	154	 74% 19% • 6%
1	B	154	 77% 15% 8%
1	C	154	 77% 16% • 6%
1	D	154	 77% 14% 9%
1	E	154	 75% 18% • 7%

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Mol	Chain	Length	Quality of chain
1	F	154	
1	G	154	
1	H	154	
1	I	154	
1	J	154	
1	K	154	
1	L	154	
1	M	154	
1	N	154	
1	O	154	
1	P	154	
1	Q	154	
1	R	154	
1	S	154	
1	T	154	
1	U	154	
1	V	154	
1	W	154	
1	X	154	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	S21	D	231	-	-	X	-
5	S21	F	231	-	-	X	-
5	S21	P	4	-	-	X	-
5	S21	R	1	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 27454 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Beta-hydroxyacyl-ACP dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	145	Total	C	N	O	S	0	0	0
			1121	731	184	201	5			
1	B	141	Total	C	N	O	S	0	0	0
			1094	713	180	196	5			
1	C	144	Total	C	N	O	S	0	0	0
			1116	727	184	200	5			
1	D	140	Total	C	N	O	S	0	0	0
			1075	699	176	195	5			
1	E	143	Total	C	N	O	S	0	0	0
			1109	722	182	200	5			
1	F	146	Total	C	N	O	S	0	1	0
			1136	736	188	207	5			
1	G	145	Total	C	N	O	S	0	0	0
			1111	722	183	201	5			
1	H	141	Total	C	N	O	S	0	0	0
			1090	710	179	196	5			
1	I	143	Total	C	N	O	S	0	1	0
			1118	732	183	198	5			
1	J	144	Total	C	N	O	S	0	0	0
			1098	714	180	199	5			
1	K	145	Total	C	N	O	S	0	0	0
			1123	731	184	203	5			
1	L	146	Total	C	N	O	S	0	0	0
			1124	728	186	205	5			
1	M	145	Total	C	N	O	S	0	0	0
			1123	731	184	203	5			
1	N	145	Total	C	N	O	S	0	0	0
			1114	724	184	201	5			
1	O	144	Total	C	N	O	S	0	0	0
			1116	727	184	200	5			
1	P	145	Total	C	N	O	S	0	0	0
			1099	714	181	199	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	142	Total	C	N	O	S	0	0	0
			1103	719	181	198	5			
1	R	146	Total	C	N	O	S	0	0	0
			1127	731	186	205	5			
1	S	146	Total	C	N	O	S	0	1	0
			1133	740	184	204	5			
1	T	142	Total	C	N	O	S	0	0	0
			1098	715	181	197	5			
1	U	144	Total	C	N	O	S	0	0	0
			1116	727	184	200	5			
1	V	144	Total	C	N	O	S	0	0	0
			1098	713	180	200	5			
1	W	142	Total	C	N	O	S	0	0	0
			1103	719	181	198	5			
1	X	145	Total	C	N	O	S	0	0	0
			1119	727	185	202	5			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	77	GLY	-	expression tag	UNP Q965D7
A	78	SER	-	expression tag	UNP Q965D7
A	79	HIS	-	expression tag	UNP Q965D7
A	80	MET	-	expression tag	UNP Q965D7
B	77	GLY	-	expression tag	UNP Q965D7
B	78	SER	-	expression tag	UNP Q965D7
B	79	HIS	-	expression tag	UNP Q965D7
B	80	MET	-	expression tag	UNP Q965D7
C	77	GLY	-	expression tag	UNP Q965D7
C	78	SER	-	expression tag	UNP Q965D7
C	79	HIS	-	expression tag	UNP Q965D7
C	80	MET	-	expression tag	UNP Q965D7
D	77	GLY	-	expression tag	UNP Q965D7
D	78	SER	-	expression tag	UNP Q965D7
D	79	HIS	-	expression tag	UNP Q965D7
D	80	MET	-	expression tag	UNP Q965D7
E	77	GLY	-	expression tag	UNP Q965D7
E	78	SER	-	expression tag	UNP Q965D7
E	79	HIS	-	expression tag	UNP Q965D7
E	80	MET	-	expression tag	UNP Q965D7
F	77	GLY	-	expression tag	UNP Q965D7
F	78	SER	-	expression tag	UNP Q965D7
F	79	HIS	-	expression tag	UNP Q965D7

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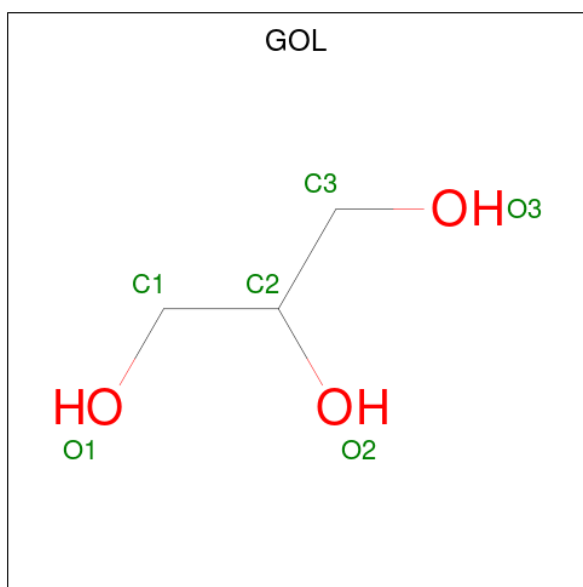
Chain	Residue	Modelled	Actual	Comment	Reference
F	80	MET	-	expression tag	UNP Q965D7
G	77	GLY	-	expression tag	UNP Q965D7
G	78	SER	-	expression tag	UNP Q965D7
G	79	HIS	-	expression tag	UNP Q965D7
G	80	MET	-	expression tag	UNP Q965D7
H	77	GLY	-	expression tag	UNP Q965D7
H	78	SER	-	expression tag	UNP Q965D7
H	79	HIS	-	expression tag	UNP Q965D7
H	80	MET	-	expression tag	UNP Q965D7
I	77	GLY	-	expression tag	UNP Q965D7
I	78	SER	-	expression tag	UNP Q965D7
I	79	HIS	-	expression tag	UNP Q965D7
I	80	MET	-	expression tag	UNP Q965D7
J	77	GLY	-	expression tag	UNP Q965D7
J	78	SER	-	expression tag	UNP Q965D7
J	79	HIS	-	expression tag	UNP Q965D7
J	80	MET	-	expression tag	UNP Q965D7
K	77	GLY	-	expression tag	UNP Q965D7
K	78	SER	-	expression tag	UNP Q965D7
K	79	HIS	-	expression tag	UNP Q965D7
K	80	MET	-	expression tag	UNP Q965D7
L	77	GLY	-	expression tag	UNP Q965D7
L	78	SER	-	expression tag	UNP Q965D7
L	79	HIS	-	expression tag	UNP Q965D7
L	80	MET	-	expression tag	UNP Q965D7
M	77	GLY	-	expression tag	UNP Q965D7
M	78	SER	-	expression tag	UNP Q965D7
M	79	HIS	-	expression tag	UNP Q965D7
M	80	MET	-	expression tag	UNP Q965D7
N	77	GLY	-	expression tag	UNP Q965D7
N	78	SER	-	expression tag	UNP Q965D7
N	79	HIS	-	expression tag	UNP Q965D7
N	80	MET	-	expression tag	UNP Q965D7
O	77	GLY	-	expression tag	UNP Q965D7
O	78	SER	-	expression tag	UNP Q965D7
O	79	HIS	-	expression tag	UNP Q965D7
O	80	MET	-	expression tag	UNP Q965D7
P	77	GLY	-	expression tag	UNP Q965D7
P	78	SER	-	expression tag	UNP Q965D7
P	79	HIS	-	expression tag	UNP Q965D7
P	80	MET	-	expression tag	UNP Q965D7
Q	77	GLY	-	expression tag	UNP Q965D7

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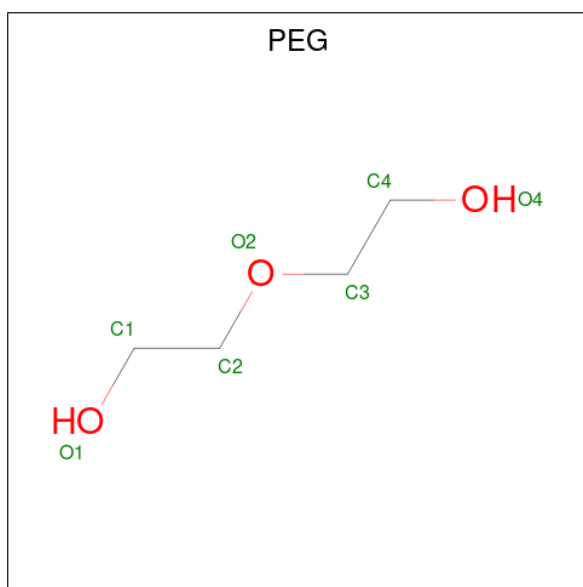
Chain	Residue	Modelled	Actual	Comment	Reference
Q	78	SER	-	expression tag	UNP Q965D7
Q	79	HIS	-	expression tag	UNP Q965D7
Q	80	MET	-	expression tag	UNP Q965D7
R	77	GLY	-	expression tag	UNP Q965D7
R	78	SER	-	expression tag	UNP Q965D7
R	79	HIS	-	expression tag	UNP Q965D7
R	80	MET	-	expression tag	UNP Q965D7
S	77	GLY	-	expression tag	UNP Q965D7
S	78	SER	-	expression tag	UNP Q965D7
S	79	HIS	-	expression tag	UNP Q965D7
S	80	MET	-	expression tag	UNP Q965D7
T	77	GLY	-	expression tag	UNP Q965D7
T	78	SER	-	expression tag	UNP Q965D7
T	79	HIS	-	expression tag	UNP Q965D7
T	80	MET	-	expression tag	UNP Q965D7
U	77	GLY	-	expression tag	UNP Q965D7
U	78	SER	-	expression tag	UNP Q965D7
U	79	HIS	-	expression tag	UNP Q965D7
U	80	MET	-	expression tag	UNP Q965D7
V	77	GLY	-	expression tag	UNP Q965D7
V	78	SER	-	expression tag	UNP Q965D7
V	79	HIS	-	expression tag	UNP Q965D7
V	80	MET	-	expression tag	UNP Q965D7
W	77	GLY	-	expression tag	UNP Q965D7
W	78	SER	-	expression tag	UNP Q965D7
W	79	HIS	-	expression tag	UNP Q965D7
W	80	MET	-	expression tag	UNP Q965D7
X	77	GLY	-	expression tag	UNP Q965D7
X	78	SER	-	expression tag	UNP Q965D7
X	79	HIS	-	expression tag	UNP Q965D7
X	80	MET	-	expression tag	UNP Q965D7

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		
2	F	1	Total	C	O	0	0
			6	3	3		
2	H	1	Total	C	O	0	0
			6	3	3		
2	I	1	Total	C	O	0	0
			6	3	3		
2	L	1	Total	C	O	0	0
			6	3	3		
2	M	1	Total	C	O	0	0
			6	3	3		
2	O	1	Total	C	O	0	0
			6	3	3		
2	P	1	Total	C	O	0	0
			6	3	3		
2	R	1	Total	C	O	0	0
			6	3	3		
2	S	1	Total	C	O	0	0
			6	3	3		
2	U	1	Total	C	O	0	0
			6	3	3		
2	W	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		
3	A	1	Total	C	O	0	0
			7	4	3		
3	A	1	Total	C	O	0	0
			7	4	3		
3	A	1	Total	C	O	0	0
			7	4	3		
3	B	1	Total	C	O	0	0
			7	4	3		
3	C	1	Total	C	O	0	0
			7	4	3		
3	E	1	Total	C	O	0	0
			7	4	3		
3	F	1	Total	C	O	0	0
			7	4	3		
3	F	1	Total	C	O	0	0
			7	4	3		
3	F	1	Total	C	O	0	0
			7	4	3		
3	G	1	Total	C	O	0	0
			7	4	3		
3	H	1	Total	C	O	0	0
			7	4	3		
3	I	1	Total	C	O	0	0
			7	4	3		
3	I	1	Total	C	O	0	0
			7	4	3		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	N	1	Total C O 7 4 3	0	0
3	O	1	Total C O 7 4 3	0	0
3	O	1	Total C O 7 4 3	0	0
3	O	1	Total C O 7 4 3	0	0
3	O	1	Total C O 7 4 3	0	0
3	Q	1	Total C O 7 4 3	0	0
3	Q	1	Total C O 7 4 3	0	0
3	Q	1	Total C O 7 4 3	0	0
3	R	1	Total C O 7 4 3	0	0
3	R	1	Total C O 7 4 3	0	0
3	S	1	Total C O 7 4 3	0	0
3	S	1	Total C O 7 4 3	0	0
3	S	1	Total C O 7 4 3	0	0
3	S	1	Total C O 7 4 3	0	0
3	U	1	Total C O 7 4 3	0	0

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

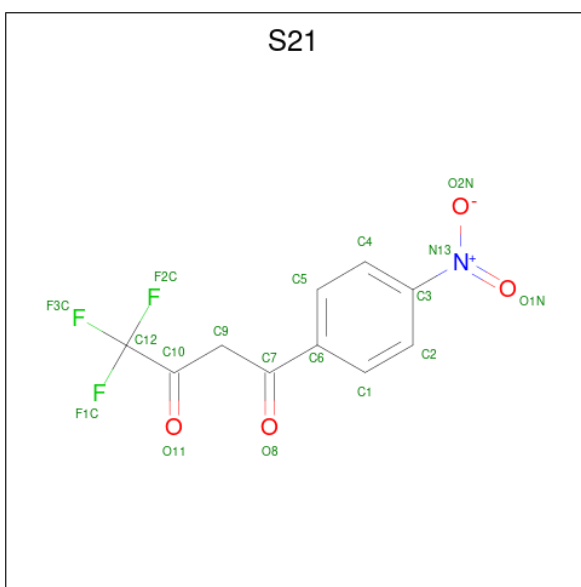
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Cl 1 1	0	0
4	B	1	Total Cl 1 1	0	0
4	C	1	Total Cl 1 1	0	0
4	G	1	Total Cl 1 1	0	0

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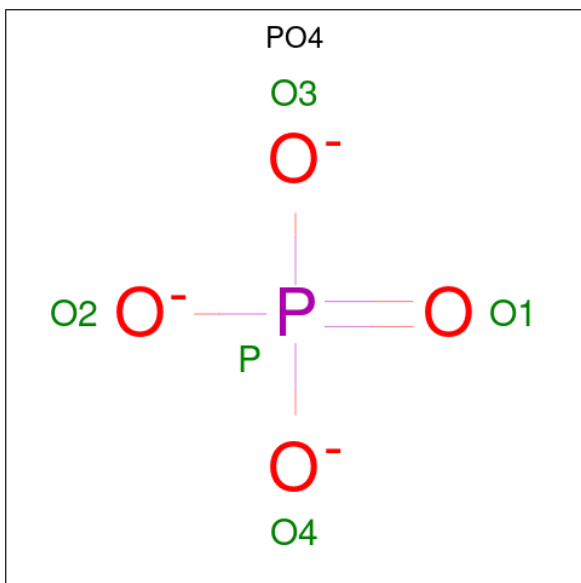
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	H	1	Total 1	Cl 1	0	0
4	I	1	Total 1	Cl 1	0	0
4	J	1	Total 1	Cl 1	0	0
4	K	1	Total 1	Cl 1	0	0
4	L	1	Total 1	Cl 1	0	0
4	M	1	Total 1	Cl 1	0	0
4	N	1	Total 1	Cl 1	0	0
4	O	1	Total 1	Cl 1	0	0
4	R	1	Total 1	Cl 1	0	0
4	S	1	Total 1	Cl 1	0	0
4	T	1	Total 1	Cl 1	0	0
4	U	1	Total 1	Cl 1	0	0
4	V	1	Total 1	Cl 1	0	0

- Molecule 5 is 4,4,4-trifluoro-1-(4-nitrophenyl)butane-1,3-dione (CCD ID: S21) (formula: C₁₀H₆F₃NO₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	D	1	Total	C	F	N	O	0	0
			18	10	3	1	4		
5	F	1	Total	C	F	N	O	0	0
			18	10	3	1	4		
5	P	1	Total	C	F	N	O	0	0
			18	10	3	1	4		
5	R	1	Total	C	F	N	O	0	0
			18	10	3	1	4		

- Molecule 6 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	E	1	Total	O	P	0	0
			5	4	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	10	Total	O		0	0
			10	10			
7	B	21	Total	O		0	0
			21	21			
7	C	27	Total	O		0	0
			27	27			
7	D	19	Total	O		0	0
			19	19			
7	E	21	Total	O		0	0
			21	21			
7	F	25	Total	O		0	0
			25	25			
7	G	18	Total	O		0	0
			18	18			
7	H	16	Total	O		0	0
			16	16			
7	I	10	Total	O		0	0
			10	10			
7	J	23	Total	O		0	0
			23	23			
7	K	12	Total	O		0	0
			12	12			
7	L	15	Total	O		0	0
			15	15			
7	M	9	Total	O		0	0
			9	9			
7	N	18	Total	O		0	0
			18	18			
7	O	19	Total	O		0	0
			19	19			
7	P	22	Total	O		0	0
			22	22			
7	Q	16	Total	O		0	0
			16	16			
7	R	26	Total	O		0	0
			26	26			
7	S	9	Total	O		0	0
			9	9			

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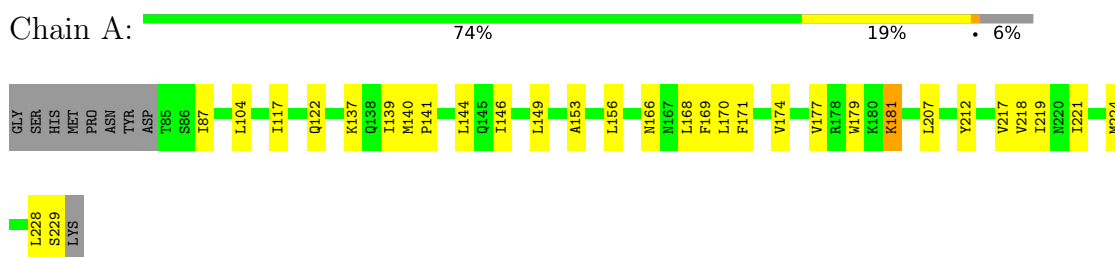
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	T	19	Total 19	O 19	0	0
7	U	18	Total 18	O 18	0	0
7	V	13	Total 13	O 13	0	0
7	W	12	Total 12	O 12	0	0
7	X	17	Total 17	O 17	0	0

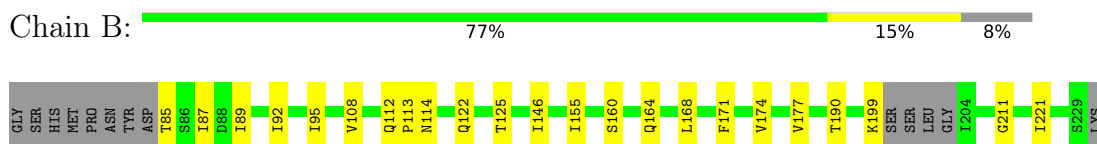
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

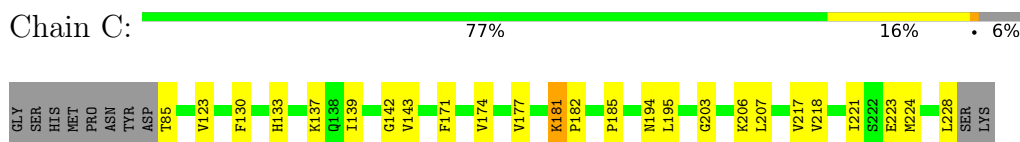
• Molecule 1: Beta-hydroxyacyl-ACP dehydratase



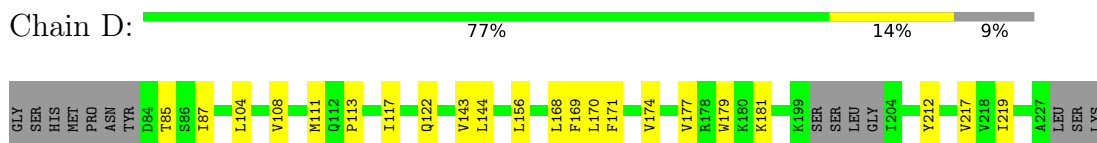
• Molecule 1: Beta-hydroxyacyl-ACP dehydratase



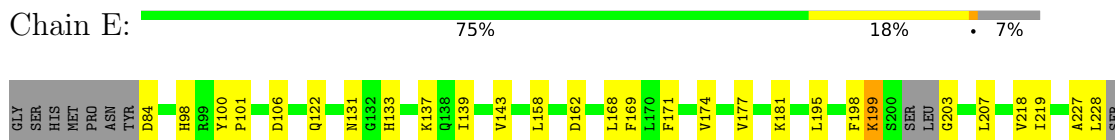
• Molecule 1: Beta-hydroxyacyl-ACP dehydratase

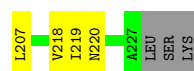


• Molecule 1: Beta-hydroxyacyl-ACP dehydratase



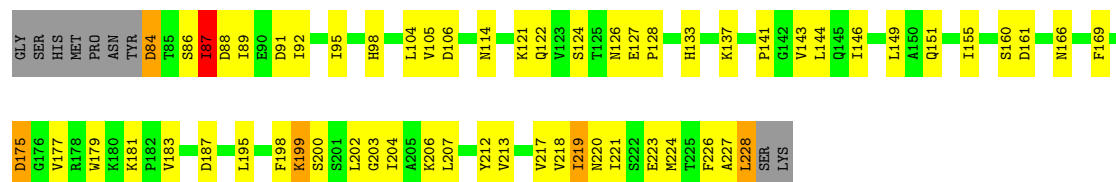
• Molecule 1: Beta-hydroxyacyl-ACP dehydratase





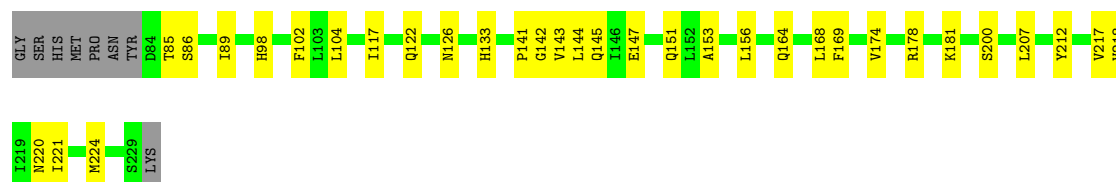
• Molecule 1: Beta-hydroxyacyl-ACP dehydratase

Chain K: 56% 34% 6%



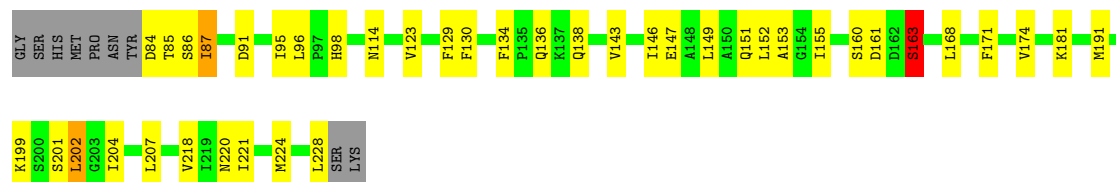
• Molecule 1: Beta-hydroxyacyl-ACP dehydratase

Chain L: 73% 21% 5%



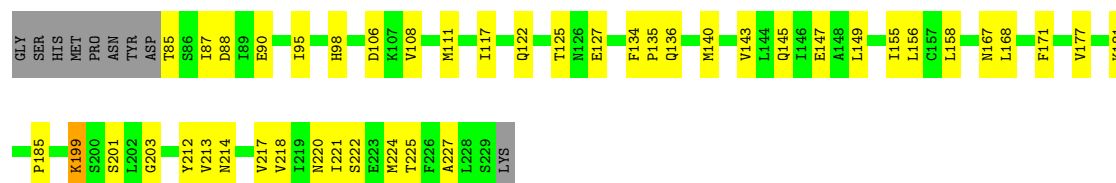
• Molecule 1: Beta-hydroxyacyl-ACP dehydratase

Chain M: 68% 25% 6%



• Molecule 1: Beta-hydroxyacyl-ACP dehydratase

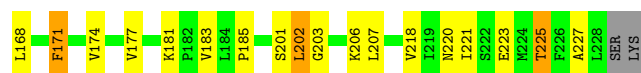
Chain N: 66% 28% 6%



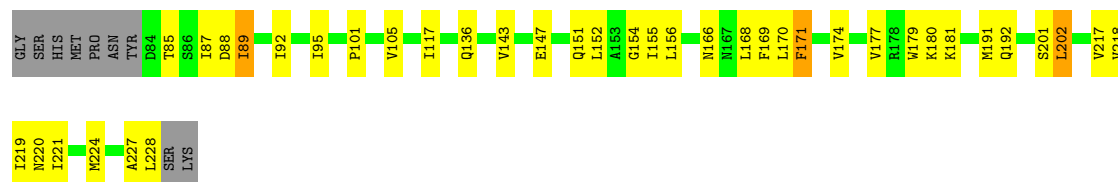
• Molecule 1: Beta-hydroxyacyl-ACP dehydratase

Chain O: 62% 26% 5% 6%

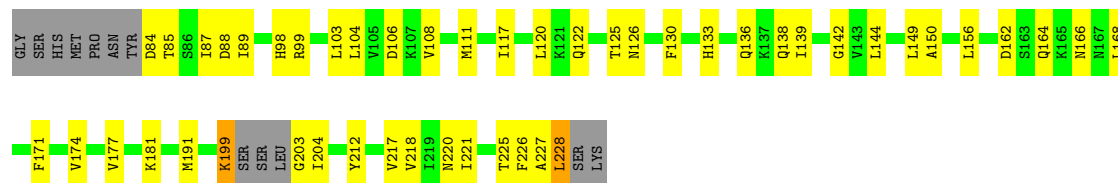




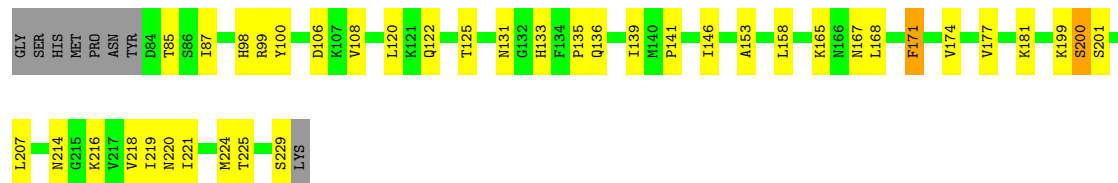
- Molecule 1: Beta-hydroxyacyl-ACP dehydratase



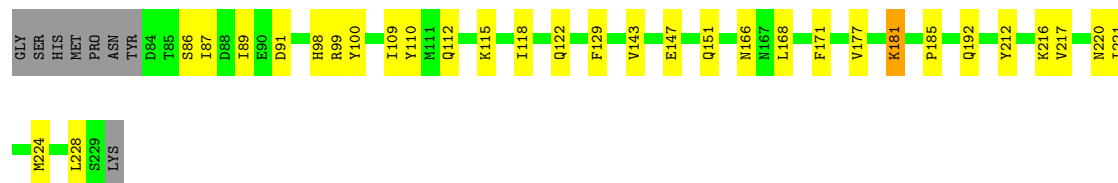
- Molecule 1: Beta-hydroxyacyl-ACP dehydratase



- Molecule 1: Beta-hydroxyacyl-ACP dehydratase



- Molecule 1: Beta-hydroxyacyl-ACP dehydratase



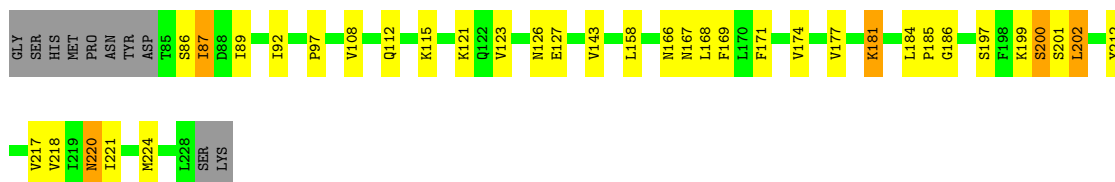
- Molecule 1: Beta-hydroxyacyl-ACP dehydratase





• Molecule 1: Beta-hydroxyacyl-ACP dehydratase

Chain U: 70% 20% 6%



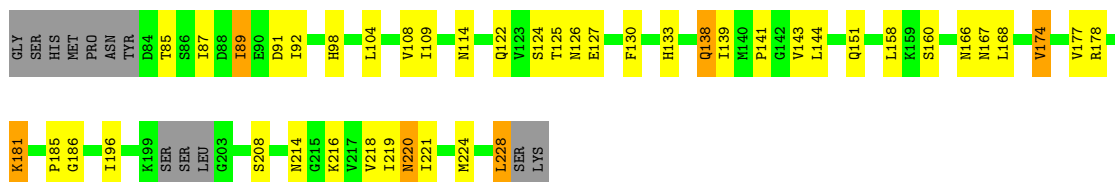
• Molecule 1: Beta-hydroxyacyl-ACP dehydratase

Chain V: 71% 21% 6%



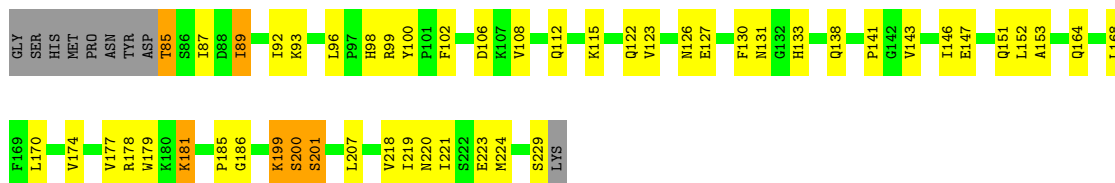
• Molecule 1: Beta-hydroxyacyl-ACP dehydratase

Chain W: 64% 25% 8%



• Molecule 1: Beta-hydroxyacyl-ACP dehydratase

Chain X: 62% 29% 6%



4 Data and refinement statistics

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, α , β , γ	218.99Å 218.99Å 157.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	51.62 – 3.10 51.62 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.4 (51.62-3.10) 99.6 (51.62-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 3.13Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.206 , 0.266 0.202 , 0.262	Depositor DCC
R_{free} test set	3395 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	63.8	Xtriage
Anisotropy	0.211	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 32.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.419 for -k,-h,-l	Xtriage
Reported twinning fraction	0.558 for H, K, L 0.442 for -H, K, -L	Depositor
Outliers	0 of 66978 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	27454	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.61 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.6688e-04.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, PEG, S21, GOL, CL

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.66	0/1143	0.86	0/1546
1	B	0.69	0/1115	0.83	0/1508
1	C	0.64	0/1138	0.81	0/1539
1	D	0.64	0/1096	0.86	0/1485
1	E	0.62	0/1130	0.85	0/1528
1	F	0.69	0/1158	0.86	2/1566 (0.1%)
1	G	0.82	0/1132	0.93	1/1533 (0.1%)
1	H	0.73	0/1111	0.87	2/1504 (0.1%)
1	I	0.64	0/1143	0.90	3/1544 (0.2%)
1	J	0.77	1/1120 (0.1%)	0.87	0/1520
1	K	0.74	0/1145	0.88	2/1550 (0.1%)
1	L	0.65	0/1146	0.88	0/1550
1	M	0.71	0/1145	0.89	1/1550 (0.1%)
1	N	0.64	0/1136	0.90	0/1538
1	O	0.65	1/1138 (0.1%)	0.88	5/1539 (0.3%)
1	P	0.67	0/1121	0.89	2/1520 (0.1%)
1	Q	0.66	0/1124	0.84	0/1520
1	R	0.67	0/1149	0.85	0/1554
1	S	0.67	0/1159	0.86	0/1569
1	T	0.75	0/1119	0.87	0/1513
1	U	0.74	1/1138 (0.1%)	0.90	2/1539 (0.1%)
1	V	0.73	0/1120	0.91	0/1519
1	W	0.86	0/1124	0.92	1/1520 (0.1%)
1	X	0.80	1/1141 (0.1%)	0.89	1/1543 (0.1%)
All	All	0.70	4/27191 (0.0%)	0.88	22/36797 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	U	166	ASN	CG-ND2	6.49	1.46	1.33
1	J	178	ARG	NE-CZ	5.62	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	X	85	THR	N-CA	5.42	1.56	1.46
1	O	165	LYS	C-N	5.36	1.41	1.33

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	U	202	LEU	N-CA-C	-7.30	103.54	114.64
1	P	89	ILE	N-CA-C	6.24	117.02	110.72
1	G	89	ILE	N-CA-C	6.22	116.96	110.62
1	K	87	ILE	N-CA-C	6.05	117.30	108.53
1	X	89	ILE	N-CA-C	5.92	117.36	110.62

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1121	0	1172	18	0
1	B	1094	0	1133	13	0
1	C	1116	0	1164	22	0
1	D	1075	0	1092	15	0
1	E	1109	0	1149	23	0
1	F	1136	0	1171	24	0
1	G	1111	0	1154	33	0
1	H	1090	0	1122	61	0
1	I	1118	0	1167	26	0
1	J	1098	0	1112	21	0
1	K	1123	0	1166	47	0
1	L	1124	0	1155	18	0
1	M	1123	0	1166	27	0
1	N	1114	0	1146	27	0
1	O	1116	0	1164	37	0
1	P	1099	0	1113	35	0
1	Q	1103	0	1144	30	0
1	R	1127	0	1164	30	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	S	1133	0	1174	26	0
1	T	1098	0	1136	40	0
1	U	1116	0	1164	24	0
1	V	1098	0	1114	20	0
1	W	1103	0	1144	42	0
1	X	1119	0	1160	38	0
2	A	6	0	8	0	0
2	D	6	0	8	0	0
2	F	6	0	8	2	0
2	H	6	0	8	2	0
2	I	6	0	8	0	0
2	L	6	0	8	0	0
2	M	6	0	8	1	0
2	O	6	0	8	1	0
2	P	6	0	8	1	0
2	R	6	0	8	0	0
2	S	6	0	8	2	0
2	U	6	0	8	0	0
2	W	6	0	8	0	0
3	A	28	0	40	0	0
3	B	7	0	10	0	0
3	C	7	0	10	0	0
3	E	7	0	10	0	0
3	F	21	0	30	3	0
3	G	7	0	10	0	0
3	H	7	0	10	0	0
3	I	14	0	20	1	0
3	N	7	0	10	0	0
3	O	28	0	40	6	0
3	Q	21	0	30	1	0
3	R	14	0	20	0	0
3	S	28	0	40	8	0
3	U	7	0	10	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	G	1	0	0	1	0
4	H	1	0	0	0	0
4	I	1	0	0	0	0
4	J	1	0	0	0	0
4	K	1	0	0	0	0
4	L	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	M	1	0	0	0	0
4	N	1	0	0	0	0
4	O	1	0	0	0	0
4	R	1	0	0	0	0
4	S	1	0	0	1	0
4	T	1	0	0	0	0
4	U	1	0	0	0	0
4	V	1	0	0	0	0
5	D	18	0	6	9	0
5	F	18	0	6	10	0
5	P	18	0	6	11	0
5	R	18	0	6	12	0
6	E	5	0	0	1	0
7	A	10	0	0	0	0
7	B	21	0	0	2	0
7	C	27	0	0	2	0
7	D	19	0	0	0	0
7	E	21	0	0	1	0
7	F	25	0	0	0	0
7	G	18	0	0	0	0
7	H	16	0	0	1	0
7	I	10	0	0	0	0
7	J	23	0	0	0	0
7	K	12	0	0	1	0
7	L	15	0	0	0	0
7	M	9	0	0	0	0
7	N	18	0	0	0	0
7	O	19	0	0	1	0
7	P	22	0	0	1	0
7	Q	16	0	0	0	0
7	R	26	0	0	0	0
7	S	9	0	0	0	0
7	T	19	0	0	0	0
7	U	18	0	0	2	0
7	V	13	0	0	0	0
7	W	12	0	0	0	0
7	X	17	0	0	1	0
All	All	27454	0	27964	605	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 605 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:171:PHE:CB	5:R:1:S21:H5	1.61	1.31
1:R:171:PHE:HB2	5:R:1:S21:C5	1.69	1.21
1:F:171:PHE:HB2	5:F:231:S21:H5	1.13	1.08
1:J:87:ILE:HG23	1:J:91:ASP:HB2	1.42	1.02
1:M:84:ASP:O	1:M:85:THR:HG22	1.62	1.00

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	143/154 (93%)	134 (94%)	9 (6%)	0	100	100
1	B	137/154 (89%)	127 (93%)	10 (7%)	0	100	100
1	C	142/154 (92%)	132 (93%)	10 (7%)	0	100	100
1	D	136/154 (88%)	127 (93%)	9 (7%)	0	100	100
1	E	139/154 (90%)	130 (94%)	9 (6%)	0	100	100
1	F	145/154 (94%)	133 (92%)	11 (8%)	1 (1%)	18	49
1	G	143/154 (93%)	133 (93%)	10 (7%)	0	100	100
1	H	137/154 (89%)	122 (89%)	15 (11%)	0	100	100
1	I	140/154 (91%)	131 (94%)	9 (6%)	0	100	100
1	J	142/154 (92%)	130 (92%)	12 (8%)	0	100	100
1	K	143/154 (93%)	134 (94%)	9 (6%)	0	100	100
1	L	144/154 (94%)	134 (93%)	10 (7%)	0	100	100
1	M	143/154 (93%)	127 (89%)	15 (10%)	1 (1%)	18	49
1	N	143/154 (93%)	131 (92%)	12 (8%)	0	100	100
1	O	142/154 (92%)	128 (90%)	14 (10%)	0	100	100
1	P	143/154 (93%)	132 (92%)	11 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	138/154 (90%)	128 (93%)	10 (7%)	0	100	100
1	R	144/154 (94%)	134 (93%)	9 (6%)	1 (1%)	18	49
1	S	145/154 (94%)	132 (91%)	13 (9%)	0	100	100
1	T	138/154 (90%)	127 (92%)	11 (8%)	0	100	100
1	U	142/154 (92%)	125 (88%)	17 (12%)	0	100	100
1	V	142/154 (92%)	130 (92%)	12 (8%)	0	100	100
1	W	138/154 (90%)	128 (93%)	10 (7%)	0	100	100
1	X	143/154 (93%)	134 (94%)	9 (6%)	0	100	100
All	All	3392/3696 (92%)	3123 (92%)	266 (8%)	3 (0%)	48	78

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	M	201	SER
1	R	200	SER
1	F	168	LEU

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	126/135 (93%)	121 (96%)	5 (4%)	28	60
1	B	122/135 (90%)	118 (97%)	4 (3%)	33	63
1	C	125/135 (93%)	122 (98%)	3 (2%)	43	69
1	D	118/135 (87%)	114 (97%)	4 (3%)	32	63
1	E	124/135 (92%)	117 (94%)	7 (6%)	19	49
1	F	127/135 (94%)	124 (98%)	3 (2%)	43	69
1	G	124/135 (92%)	117 (94%)	7 (6%)	19	49
1	H	121/135 (90%)	114 (94%)	7 (6%)	18	48
1	I	125/135 (93%)	117 (94%)	8 (6%)	16	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	J	119/135 (88%)	115 (97%)	4 (3%)	32	63
1	K	126/135 (93%)	117 (93%)	9 (7%)	13	41
1	L	125/135 (93%)	118 (94%)	7 (6%)	19	49
1	M	126/135 (93%)	117 (93%)	9 (7%)	13	41
1	N	123/135 (91%)	114 (93%)	9 (7%)	13	40
1	O	125/135 (93%)	115 (92%)	10 (8%)	11	37
1	P	119/135 (88%)	113 (95%)	6 (5%)	22	53
1	Q	123/135 (91%)	110 (89%)	13 (11%)	6	26
1	R	126/135 (93%)	117 (93%)	9 (7%)	13	41
1	S	127/135 (94%)	123 (97%)	4 (3%)	35	64
1	T	122/135 (90%)	114 (93%)	8 (7%)	15	43
1	U	125/135 (93%)	118 (94%)	7 (6%)	19	49
1	V	120/135 (89%)	115 (96%)	5 (4%)	26	58
1	W	123/135 (91%)	114 (93%)	9 (7%)	13	40
1	X	125/135 (93%)	115 (92%)	10 (8%)	11	37
All	All	2966/3240 (92%)	2799 (94%)	167 (6%)	19	49

5 of 167 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	R	85	THR
1	V	168	LEU
1	R	171	PHE
1	T	87	ILE
1	W	138	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	220	ASN
1	Q	136	GLN
1	M	112	GLN
1	O	164	GLN
1	R	145	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 64 ligands modelled in this entry, 17 are monoatomic - leaving 47 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	PEG	S	8	-	6,6,6	0.69	0	5,5,5	0.45	0
3	PEG	F	2	-	6,6,6	0.65	0	5,5,5	0.22	0
3	PEG	U	21	-	6,6,6	0.81	0	5,5,5	0.49	0
2	GOL	S	10	-	5,5,5	0.46	0	5,5,5	1.05	0
2	GOL	M	7	-	5,5,5	0.38	0	5,5,5	0.32	0
2	GOL	P	13	-	5,5,5	0.39	0	5,5,5	0.66	0
5	S21	F	231	-	18,18,18	0.88	0	22,26,26	1.21	2 (9%)
5	S21	D	231	-	18,18,18	0.92	1 (5%)	22,26,26	1.01	1 (4%)
2	GOL	I	5	-	5,5,5	0.36	0	5,5,5	0.42	0
2	GOL	H	4	-	5,5,5	0.47	0	5,5,5	0.34	0
2	GOL	U	11	-	5,5,5	0.36	0	5,5,5	0.35	0
2	GOL	F	3	-	5,5,5	0.30	0	5,5,5	0.54	0
6	PO4	E	1	-	4,4,4	0.65	0	6,6,6	0.62	0
3	PEG	Q	16	-	6,6,6	0.79	0	5,5,5	0.44	0
3	PEG	O	23	-	6,6,6	0.60	0	5,5,5	0.76	0
3	PEG	R	29	-	6,6,6	0.74	0	5,5,5	0.19	0
2	GOL	O	8	-	5,5,5	0.38	0	5,5,5	0.38	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	A	1	-	5,5,5	0.34	0	5,5,5	0.44	0
3	PEG	I	11	-	6,6,6	0.53	0	5,5,5	0.27	0
5	S21	P	4	-	18,18,18	0.81	0	22,26,26	0.91	0
3	PEG	O	10	-	6,6,6	0.57	0	5,5,5	0.38	0
2	GOL	W	12	-	5,5,5	0.31	0	5,5,5	0.45	0
3	PEG	G	6	-	6,6,6	0.59	0	5,5,5	0.41	0
2	GOL	R	9	-	5,5,5	0.33	0	5,5,5	0.44	0
3	PEG	O	28	-	6,6,6	0.44	0	5,5,5	0.31	0
3	PEG	O	22	-	6,6,6	0.63	0	5,5,5	0.27	0
3	PEG	R	15	-	6,6,6	0.54	0	5,5,5	0.48	0
3	PEG	S	19	-	6,6,6	0.69	0	5,5,5	0.21	0
3	PEG	A	27	-	6,6,6	0.64	0	5,5,5	0.32	0
3	PEG	A	5	-	6,6,6	0.59	0	5,5,5	0.26	0
3	PEG	Q	7	-	6,6,6	0.70	0	5,5,5	0.31	0
3	PEG	I	20	-	6,6,6	0.38	0	5,5,5	0.30	0
3	PEG	B	3	-	6,6,6	0.57	0	5,5,5	0.27	0
3	PEG	S	13	-	6,6,6	0.50	0	5,5,5	0.36	0
3	PEG	A	18	-	6,6,6	0.58	0	5,5,5	0.32	0
3	PEG	A	26	-	6,6,6	0.64	0	5,5,5	0.29	0
5	S21	R	1	-	18,18,18	0.75	0	22,26,26	1.12	2 (9%)
3	PEG	C	1	-	6,6,6	0.70	0	5,5,5	0.23	0
3	PEG	E	17	-	6,6,6	0.67	0	5,5,5	0.23	0
3	PEG	S	12	-	6,6,6	0.57	0	5,5,5	0.48	0
3	PEG	H	231	-	6,6,6	0.52	0	5,5,5	0.39	0
3	PEG	Q	9	-	6,6,6	0.59	0	5,5,5	0.21	0
3	PEG	F	25	-	6,6,6	0.60	0	5,5,5	0.31	0
3	PEG	N	14	-	6,6,6	0.74	0	5,5,5	0.39	0
3	PEG	F	24	-	6,6,6	0.60	0	5,5,5	0.29	0
2	GOL	D	2	-	5,5,5	0.28	0	5,5,5	0.57	0
2	GOL	L	6	-	5,5,5	0.40	0	5,5,5	0.23	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PEG	S	8	-	-	3/4/4/4	-
3	PEG	F	2	-	-	2/4/4/4	-
3	PEG	U	21	-	-	1/4/4/4	-
2	GOL	S	10	-	-	2/4/4/4	-
2	GOL	M	7	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	P	13	-	-	2/4/4/4	-
5	S21	F	231	-	-	11/16/18/18	0/1/1/1
5	S21	D	231	-	-	4/16/18/18	0/1/1/1
2	GOL	I	5	-	-	2/4/4/4	-
2	GOL	H	4	-	-	0/4/4/4	-
2	GOL	U	11	-	-	2/4/4/4	-
2	GOL	F	3	-	-	0/4/4/4	-
3	PEG	Q	16	-	-	1/4/4/4	-
3	PEG	O	23	-	-	3/4/4/4	-
3	PEG	R	29	-	-	3/4/4/4	-
2	GOL	O	8	-	-	0/4/4/4	-
2	GOL	A	1	-	-	2/4/4/4	-
3	PEG	I	11	-	-	3/4/4/4	-
5	S21	P	4	-	-	7/16/18/18	0/1/1/1
3	PEG	O	10	-	-	3/4/4/4	-
2	GOL	W	12	-	-	4/4/4/4	-
3	PEG	G	6	-	-	3/4/4/4	-
2	GOL	R	9	-	-	4/4/4/4	-
3	PEG	O	28	-	-	2/4/4/4	-
3	PEG	O	22	-	-	2/4/4/4	-
3	PEG	R	15	-	-	3/4/4/4	-
3	PEG	S	19	-	-	3/4/4/4	-
3	PEG	A	27	-	-	3/4/4/4	-
3	PEG	A	5	-	-	0/4/4/4	-
3	PEG	Q	7	-	-	2/4/4/4	-
3	PEG	I	20	-	-	3/4/4/4	-
3	PEG	B	3	-	-	4/4/4/4	-
3	PEG	S	13	-	-	3/4/4/4	-
3	PEG	A	18	-	-	4/4/4/4	-
3	PEG	A	26	-	-	3/4/4/4	-
5	S21	R	1	-	-	11/16/18/18	0/1/1/1
3	PEG	C	1	-	-	1/4/4/4	-
3	PEG	E	17	-	-	3/4/4/4	-
3	PEG	S	12	-	-	2/4/4/4	-
3	PEG	H	231	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PEG	Q	9	-	-	3/4/4/4	-
3	PEG	F	25	-	-	3/4/4/4	-
3	PEG	N	14	-	-	2/4/4/4	-
3	PEG	F	24	-	-	4/4/4/4	-
2	GOL	D	2	-	-	2/4/4/4	-
2	GOL	L	6	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	231	S21	C3-N13	-2.04	1.40	1.45

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	231	S21	C2-C3-N13	2.59	121.60	119.34
5	R	1	S21	C2-C3-N13	2.38	121.42	119.34
5	F	231	S21	C4-C3-N13	2.28	121.33	119.34
5	R	1	S21	O8-C7-C9	-2.12	118.06	120.58
5	F	231	S21	C2-C3-N13	2.06	121.14	119.34

There are no chirality outliers.

5 of 129 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	L	6	GOL	O1-C1-C2-O2
2	L	6	GOL	O1-C1-C2-C3
2	R	9	GOL	O1-C1-C2-C3
2	R	9	GOL	C1-C2-C3-O3
2	R	9	GOL	O2-C2-C3-O3

There are no ring outliers.

23 monomers are involved in 72 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	S	8	PEG	3	0
3	U	21	PEG	1	0
2	S	10	GOL	2	0
2	M	7	GOL	1	0

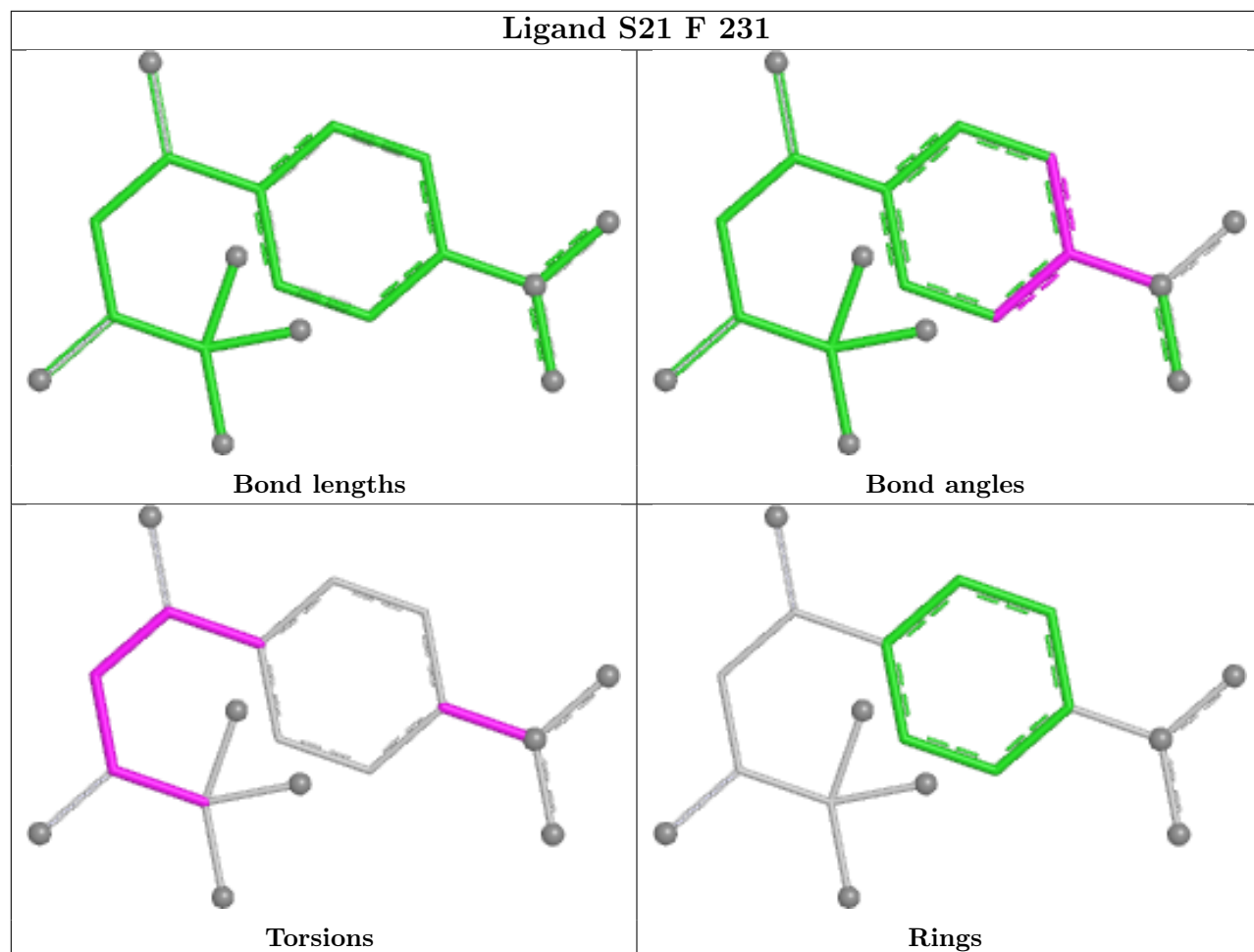
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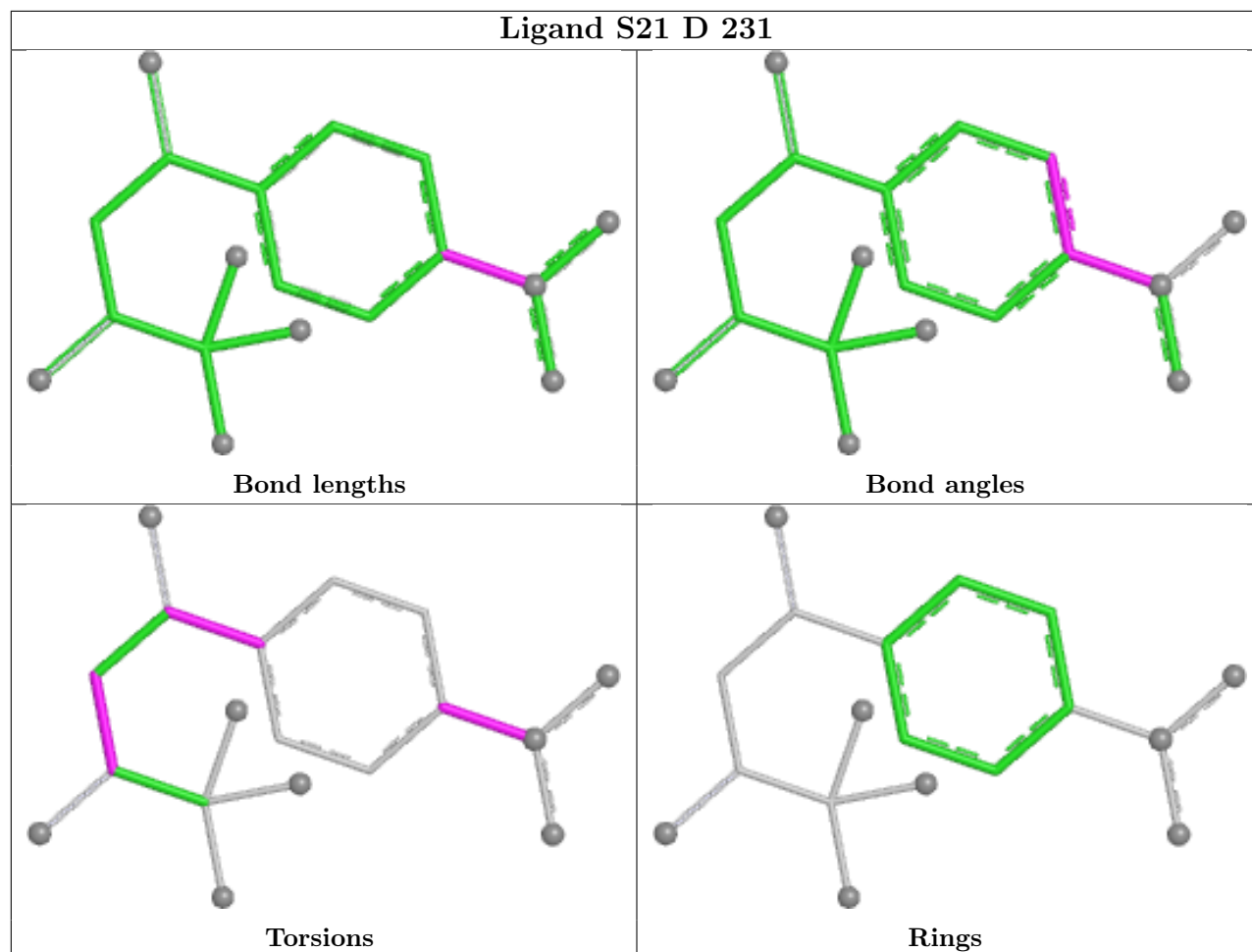
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	P	13	GOL	1	0
5	F	231	S21	10	0
5	D	231	S21	9	0
2	H	4	GOL	2	0
2	F	3	GOL	2	0
6	E	1	PO4	1	0
3	O	23	PEG	3	0
2	O	8	GOL	1	0
3	I	11	PEG	1	0
5	P	4	S21	11	0
3	O	10	PEG	1	0
3	O	28	PEG	2	0
3	S	19	PEG	1	0
3	S	13	PEG	3	0
5	R	1	S21	12	0
3	S	12	PEG	1	0
3	Q	9	PEG	1	0
3	F	25	PEG	3	0
3	F	24	PEG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

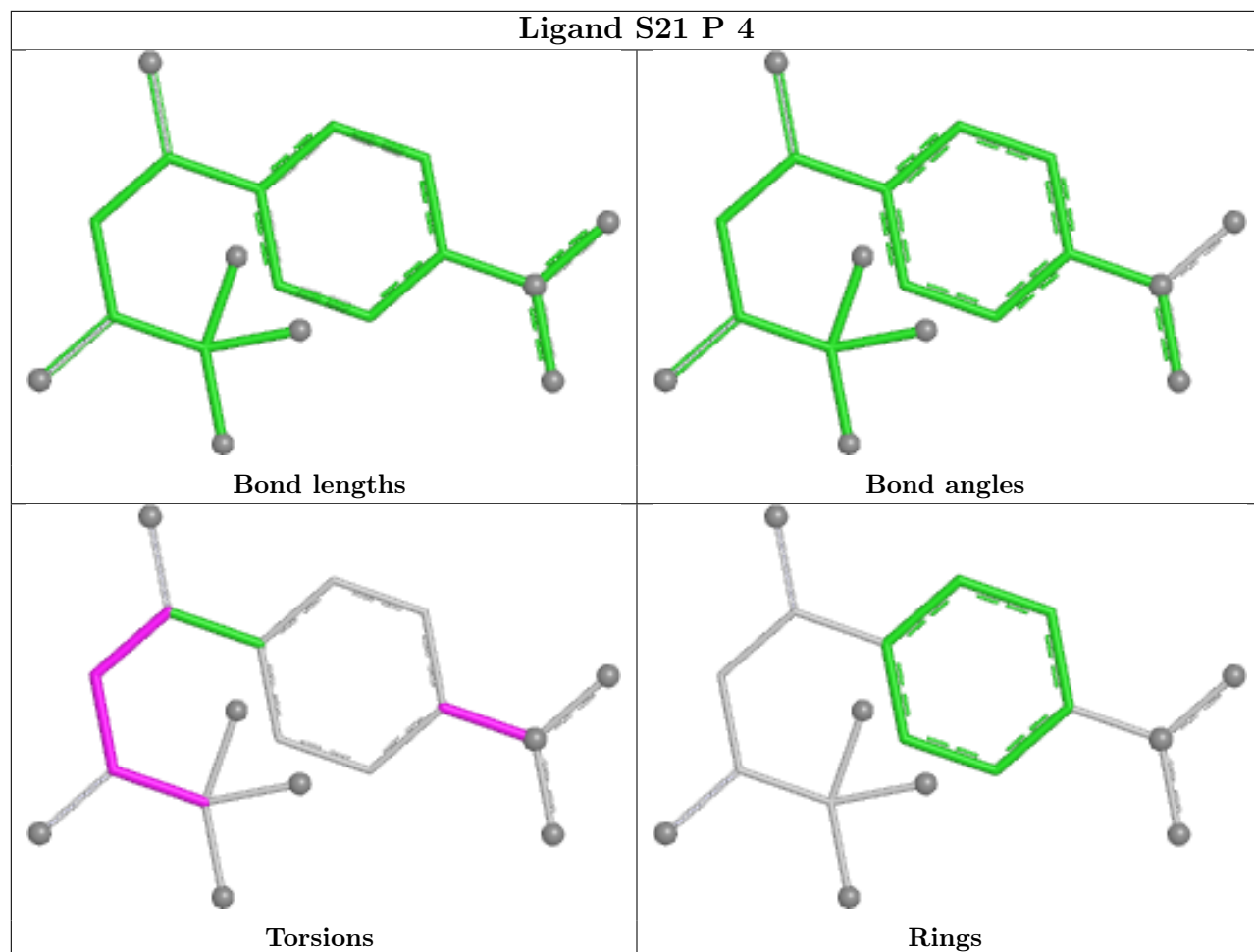
Ligand S21 F 231

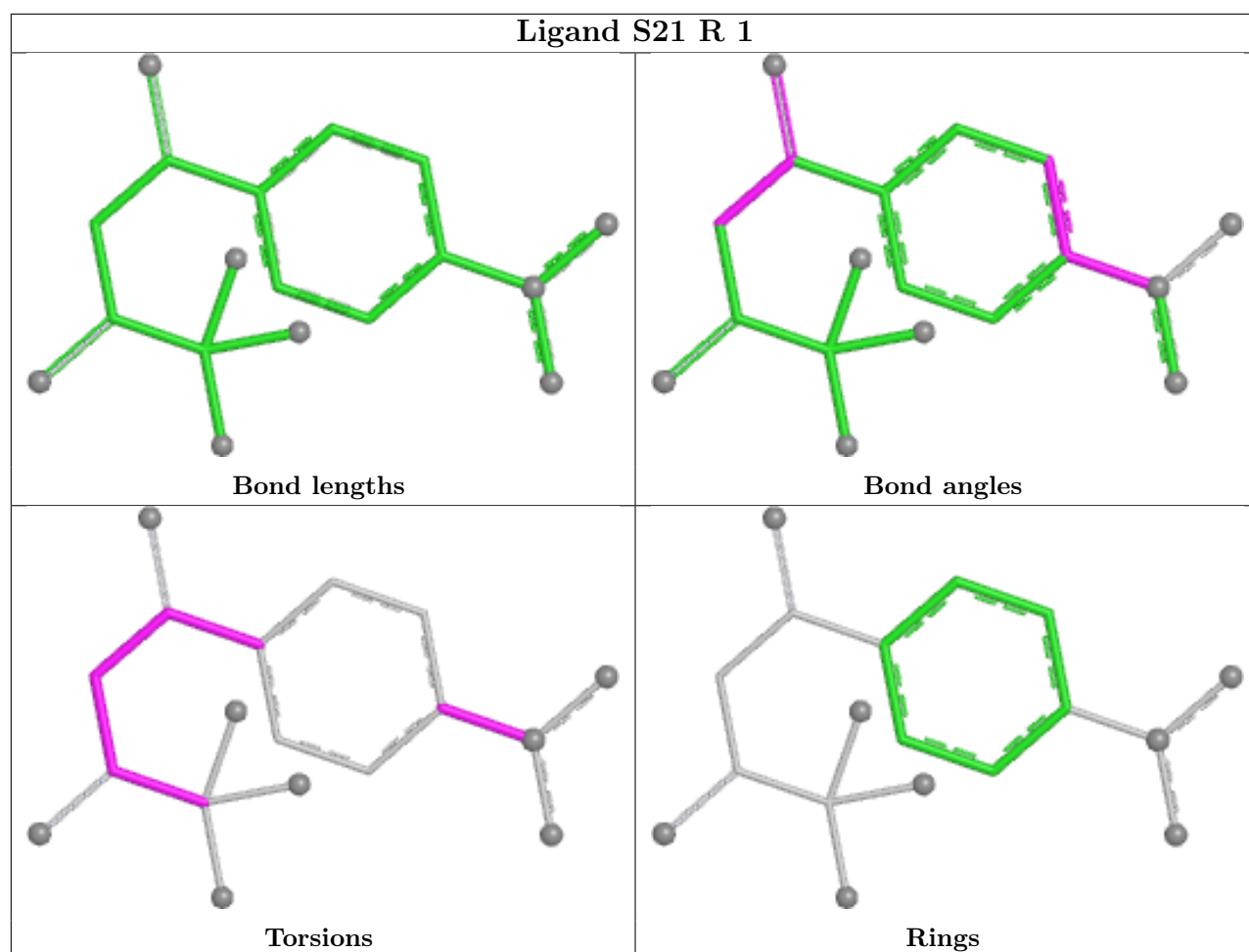


Ligand S21 D 231



Ligand S21 P 4





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	145/154 (94%)	-1.38	0 100 100	32, 56, 71, 72	0
1	B	141/154 (91%)	-1.46	0 100 100	33, 56, 72, 77	0
1	C	144/154 (93%)	-1.53	0 100 100	28, 41, 64, 70	0
1	D	140/154 (90%)	-1.48	0 100 100	32, 46, 67, 71	1 (0%)
1	E	143/154 (92%)	-1.47	0 100 100	28, 42, 65, 71	0
1	F	146/154 (94%)	-1.51	0 100 100	17, 44, 64, 73	1 (0%)
1	G	145/154 (94%)	-1.29	0 100 100	49, 61, 73, 79	0
1	H	141/154 (91%)	-1.37	0 100 100	48, 61, 74, 77	0
1	I	143/154 (92%)	-1.45	0 100 100	40, 52, 70, 77	1 (0%)
1	J	144/154 (93%)	-1.36	0 100 100	44, 59, 73, 78	1 (0%)
1	K	145/154 (94%)	-1.39	0 100 100	46, 58, 73, 78	0
1	L	146/154 (94%)	-1.41	0 100 100	42, 61, 76, 80	0
1	M	145/154 (94%)	-1.37	0 100 100	35, 55, 70, 73	0
1	N	145/154 (94%)	-1.45	0 100 100	31, 52, 70, 74	0
1	O	144/154 (93%)	-1.48	0 100 100	29, 44, 62, 68	0
1	P	145/154 (94%)	-1.43	0 100 100	33, 50, 66, 73	1 (0%)
1	Q	142/154 (92%)	-1.47	0 100 100	26, 44, 67, 73	0
1	R	146/154 (94%)	-1.47	0 100 100	30, 47, 69, 76	0
1	S	146/154 (94%)	-1.43	0 100 100	39, 50, 71, 78	1 (0%)
1	T	142/154 (92%)	-1.37	0 100 100	41, 59, 73, 79	0
1	U	144/154 (93%)	-1.43	0 100 100	41, 57, 71, 76	0
1	V	144/154 (93%)	-1.41	0 100 100	40, 55, 74, 79	1 (0%)
1	W	142/154 (92%)	-1.33	0 100 100	48, 63, 78, 85	0
1	X	145/154 (94%)	-1.34	0 100 100	46, 62, 77, 81	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	3453/3696 (93%)	-1.42	0 100 100	17, 54, 72, 85	7 (0%)

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	PEG	A	5	7/7	0.90	0.09	57,58,58,59	0
3	PEG	F	25	7/7	0.90	0.08	63,63,64,64	0
3	PEG	F	2	7/7	0.96	0.05	42,42,43,43	0
3	PEG	E	17	7/7	0.96	0.05	59,60,60,60	0
3	PEG	Q	7	7/7	0.96	0.05	56,58,59,59	0
3	PEG	Q	16	7/7	0.97	0.04	48,49,50,50	0
4	CL	B	4	1/1	0.97	0.04	49,49,49,49	0
2	GOL	L	6	6/6	0.98	0.05	35,38,38,39	0
3	PEG	A	18	7/7	0.98	0.04	53,56,58,58	0
3	PEG	F	24	7/7	0.98	0.04	38,41,42,42	0
3	PEG	A	26	7/7	0.98	0.04	51,52,53,53	0
3	PEG	G	6	7/7	0.98	0.04	29,29,30,30	0
3	PEG	N	14	7/7	0.98	0.04	29,34,35,36	0
3	PEG	O	23	7/7	0.98	0.04	27,32,37,38	0
3	PEG	A	27	7/7	0.98	0.04	52,54,55,55	0
3	PEG	Q	9	7/7	0.98	0.04	40,41,42,42	0
3	PEG	B	3	7/7	0.98	0.04	40,41,41,41	0
3	PEG	R	15	7/7	0.98	0.04	36,40,43,44	0
3	PEG	R	29	7/7	0.98	0.04	40,43,43,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	PEG	S	8	7/7	0.98	0.06	55,56,56,56	0
3	PEG	S	12	7/7	0.98	0.04	28,28,30,31	0
3	PEG	U	21	7/7	0.98	0.05	37,40,41,42	0
3	PEG	C	1	7/7	0.98	0.04	36,37,39,39	0
4	CL	L	11	1/1	0.98	0.04	50,50,50,50	0
4	CL	N	13	1/1	0.98	0.08	66,66,66,66	0
3	PEG	I	11	7/7	0.99	0.04	51,51,53,53	0
3	PEG	I	20	7/7	0.99	0.06	74,74,74,75	0
2	GOL	W	12	6/6	0.99	0.05	54,55,55,56	0
3	PEG	O	10	7/7	0.99	0.06	46,47,48,48	0
3	PEG	O	22	7/7	0.99	0.04	52,53,54,55	0
2	GOL	D	2	6/6	0.99	0.04	29,30,30,30	0
3	PEG	O	28	7/7	0.99	0.06	29,30,32,33	0
2	GOL	F	3	6/6	0.99	0.04	27,29,29,29	0
2	GOL	H	4	6/6	0.99	0.04	25,28,29,29	0
2	GOL	I	5	6/6	0.99	0.07	58,59,60,60	0
2	GOL	A	1	6/6	0.99	0.04	45,46,46,46	0
2	GOL	M	7	6/6	0.99	0.04	29,30,30,31	0
2	GOL	O	8	6/6	0.99	0.05	23,24,25,26	0
2	GOL	P	13	6/6	0.99	0.03	27,30,30,31	0
3	PEG	S	13	7/7	0.99	0.04	46,47,47,48	0
3	PEG	S	19	7/7	0.99	0.05	34,37,39,39	0
2	GOL	R	9	6/6	0.99	0.03	28,29,31,33	0
4	CL	A	3	1/1	0.99	0.04	55,55,55,55	0
2	GOL	S	10	6/6	0.99	0.05	36,37,38,39	0
4	CL	C	5	1/1	0.99	0.07	51,51,51,51	0
4	CL	G	7	1/1	0.99	0.02	57,57,57,57	0
4	CL	J	9	1/1	0.99	0.04	49,49,49,49	0
4	CL	K	10	1/1	0.99	0.04	53,53,53,53	0
2	GOL	U	11	6/6	0.99	0.04	40,41,42,43	0
4	CL	M	12	1/1	0.99	0.03	39,39,39,39	0
3	PEG	H	231	7/7	0.99	0.03	52,52,55,55	0
4	CL	O	1	1/1	0.99	0.03	45,45,45,45	0
4	CL	R	14	1/1	0.99	0.04	54,54,54,54	0
4	CL	S	15	1/1	0.99	0.04	43,43,43,43	0
4	CL	T	16	1/1	0.99	0.04	50,50,50,50	0
4	CL	V	17	1/1	0.99	0.05	39,39,39,39	0
5	S21	D	231	18/18	0.99	0.04	50,55,57,57	0
5	S21	F	231	18/18	0.99	0.05	66,70,73,73	6
5	S21	P	4	18/18	0.99	0.04	63,65,66,67	0
5	S21	R	1	18/18	0.99	0.03	44,46,52,53	0
6	PO4	E	1	5/5	0.99	0.04	42,43,44,44	0

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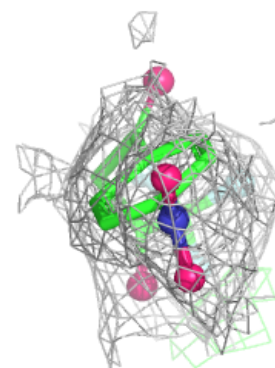
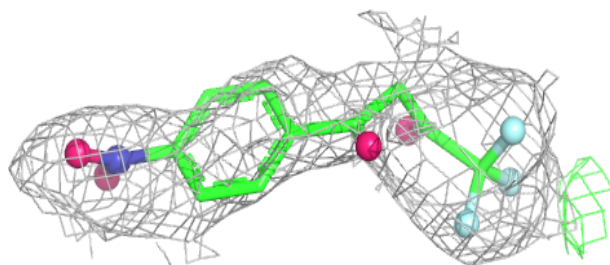
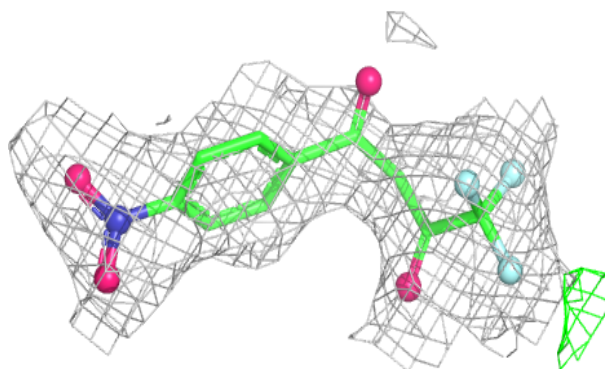
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CL	I	8	1/1	1.00	0.02	46,46,46,46	0
4	CL	H	6	1/1	1.00	0.01	44,44,44,44	0
4	CL	U	2	1/1	1.00	0.04	52,52,52,52	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

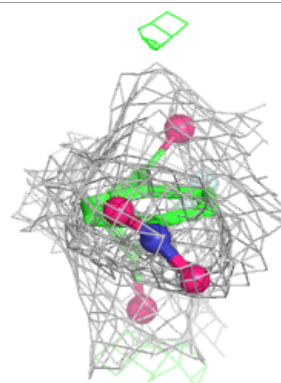
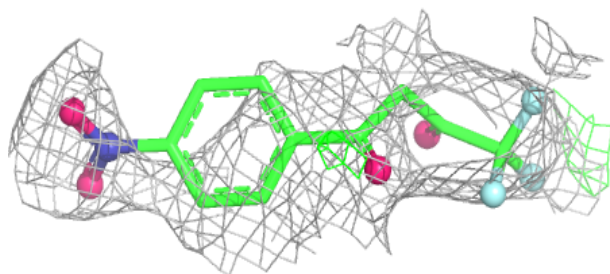
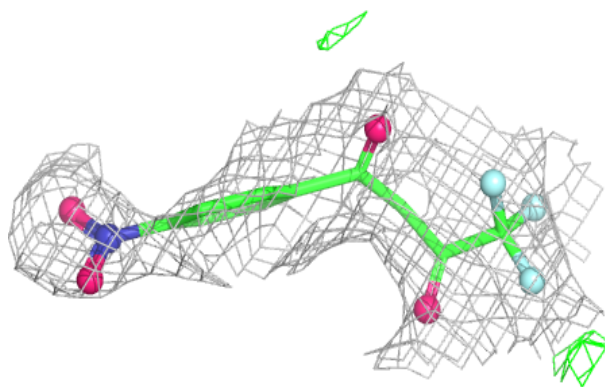
Electron density around S21 D 231:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

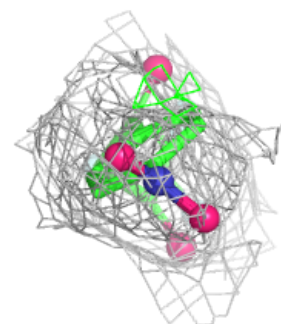
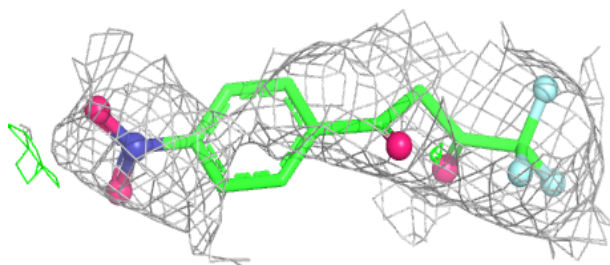
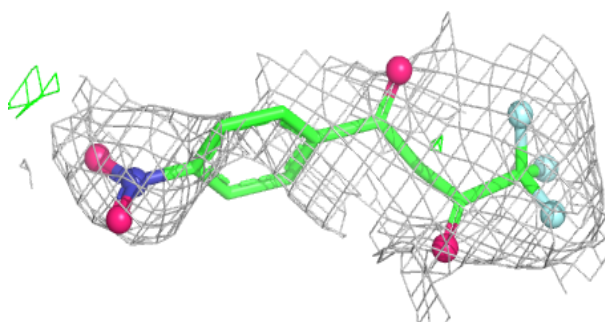


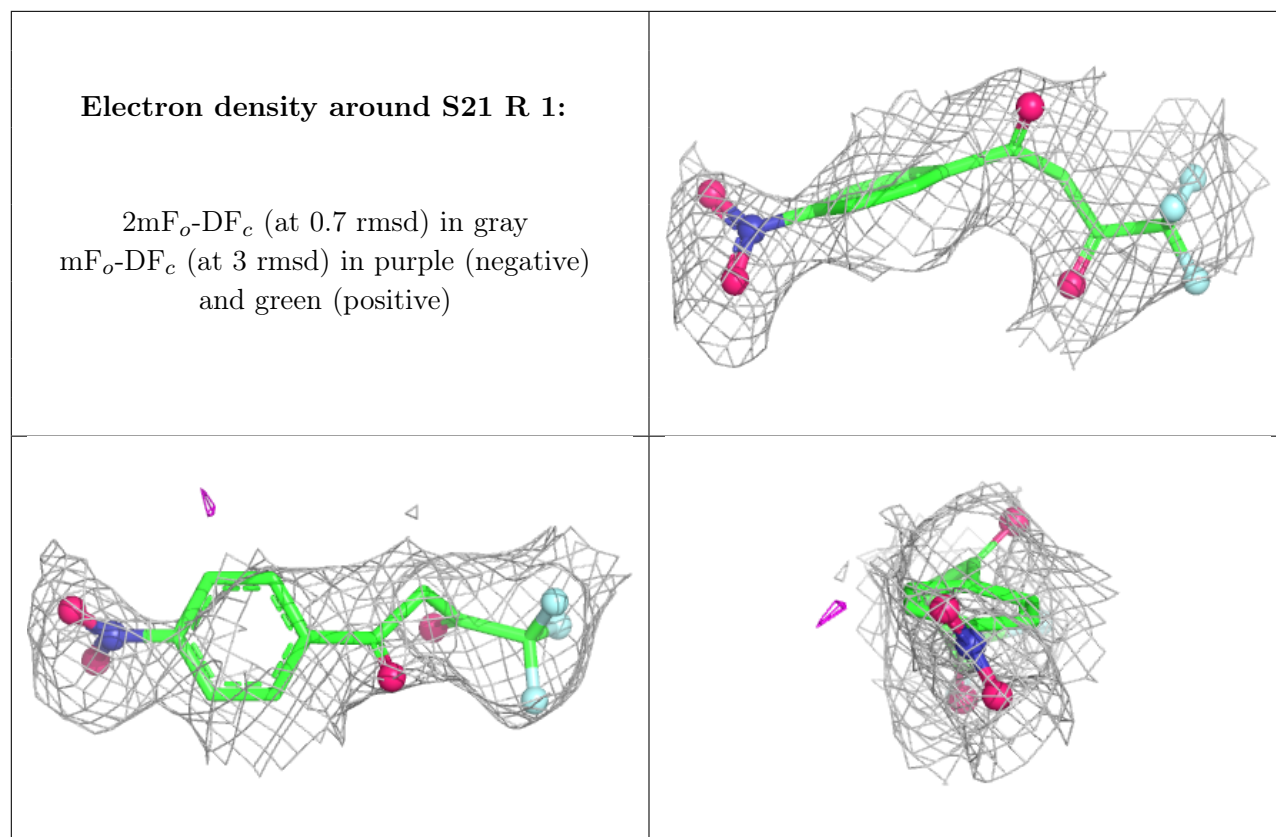
Electron density around S21 F 231:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around S21 P 4:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.